Amendments to the Claims

Please amend the claims in the application as shown below in the list of claims.

List of Claims

1-20. Cancelled.

21. (Previously presented) A process for the production of an L-amino acid comprising:

a) culturing a recombinant microorganism from the Enterobacteriaceae family in a fermentation medium, wherein;

i) said recombinant microorganism produces said L-amino acid;

ii) said recombinant microorganism has been transformed with a vector comprising an open reading frame (ORF) that encodes a protein comprising the amino acid sequence of SEQ ID NO:4;

iii) said ORF is overexpressed in said recombinant microorganism by increasing the copy number of said ORF or by linking said ORF to a promoter;

b) allowing said fermentation medium or said recombinant microorganism to become enriched in said L-amino acid; and

c) isolating said L-amino acid.

22. (Currently amended) The process of claim 21, wherein said ORF encodes a protein that consists of the amino acid sequence of SEQ ID NO:4.

23. (Previously presented) The process of claim 21 wherein some or all of the constituents of said fermentation medium and/or the biomass of said recombinant microorganism are isolated with said L-amino acid.

24. (Previously presented) The process of claim 21 wherein said ORF that encodes a protein with the amino acid sequence of SEQ ID NO:4 comprises the nucleotide sequence of SEQ ID NO:3.

25. (Previously presented) The process of claim 24 wherein said ORF that encodes a protein with the amino acid sequence of SEQ ID NO:4 consists of the nucleotide sequence of SEQ ID NO:3.

26. (Previously presented) The process of claim 21, wherein the genus of said recombinant microorganism is selected from the group consisting of: Escherichia; Erwinia; Providencia; and Serratia.

27. (Currently amended) The process of claim 21, wherein said microorganism overexpresses said ORF and, in addition, the activity of one or more additional ~~*E. coli*~~ genes is overexpressed, said one or more additional genes being selected from the group consisting of:

a) the *E. coli* thrABC operon coding for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase;
b) the *C. glutamicum* pyc gene coding for pyruvate carboxylase;
c) the *E. coli* pps gene for phosphoenolpyruvate synthase;
d) the *E. coli* ppc gene coding for phosphoenolpyruvate carboxylase;
e) the *E. coli* genes pntA and pntB coding for transhydrogenase;
f) the *E. coli* rhtB gene imparting homoserine resistance;
g) the *E. coli* mqo gene coding for malate:quinone oxidoreductase;
h) the *E. coli* rhtC gene imparting threonine resistance;
i) the *C. glutamicum* thrE gene coding for the threonine-export protein;
j) the *E. coli* gdhA gene coding for glutamate dehydrogenase;
k) the *E. coli* hns gene coding for the DNA binding protein HLP-II;
l) the *E. coli* pgm gene coding for phosphoglucomutase;
m) the *E. coli* fba gene coding for fructose biphosphate aldolase;
n) the *E. coli* ptsH gene coding for phosphohistidine protein hexose phosphotransferase;
o) the *E. coli* ptsI gene coding for enzyme I of the phosphotransferase system;
p) the *E. coli* crr gene coding for the glucose-specific IIA component;
q) the *E. coli* ptsG gene coding for the glucose-specific IIBC component;

r) the *E. coli* lrp gene coding for the regulator of the leucine regulon;

s) the *E. coli* csrA gene coding for the global regulator Csr;

t) the *E. coli* fadR gene coding for the regulator of the fad regulon;

u) the *E. coli* iclR gene coding for the regulator of central intermediary metabolism;

v) the *E. coli* mopB gene coding for the 10 kDa chaperon;

w) the *E. coli* ahpC gene coding for the small subunit of alkyl hydroperoxide reductase;

x) the *E. coli* ahpF gene coding for the large subunit of alkyl hydroperoxide reductase;

y) the *E. coli* cysK gene coding for cysteine synthase A;

z) the *E. coli* cysB gene coding for the regulator of the cys regulon;

aa) the *E. coli* cysJ gene coding for the flavoprotein of NADPH sulfite reductase;

bb) the *E. coli* cysI gene coding for the haemoprotein of NADPH sulfite reductase;

cc) the *E. coli* cysH gene coding for adenylyl sulfate reductase;

dd) the *E. coli* phoB gene coding for the positive regulator PhoB of the pho regulon;

ee) the *E. coli* phoR gene coding for the sensor protein of the pho regulon;

ff) the *E. coli* phoE gene coding for protein E of the outer cell membrane;

gg) the *E. coli* pykF gene coding for pyruvate kinase I, which is stimulated by fructose;

hh) the *E. coli* pfkB gene coding for 6-phosphofructokinase II;

ii) the *E. coli* malE gene coding for the periplasmic binding protein of maltose transport;

jj) the *E. coli* sodA gene coding for superoxide dismutase;

kk) the *E. coli* rseA gene coding for a membrane protein with anti-sigmaE activity;

ll) the *E. coli* rseC gene coding for a global regulator of the sigmaE factor;

mm) the *E. coli* sucA gene coding for the decarboxylase subunit of 2-ketoglutarate dehydrogenase;

nn) the *E. coli* sucB gene coding for the dihydrolipoyl transsuccinase E2 subunit of 2-ketoglutarate dehydrogenase;

oo) the *E. coli* sucC gene coding for the β-subunit of succinyl-CoA synthetase;

pp) the *E. coli* sucD gene coding for the α-subunit of succinyl-CoA synthetase;

qq) the *E. coli* adk gene coding for adenylate kinase;

rr) the *E. coli* hdeA gene coding for a periplasmic protein with chaperonin-type function;

ss) the *E. coli* hdeB gene coding for a periplasmic protein with chaperonin-type function;

tt) the *E. coli* icd gene coding for isocitrate dehydrogenase;

uu) the *E. coli* mglB gene coding for the periplasmic, galactose-binding transport protein;

vv) the *E. coli* lpd gene coding for dihydrolipoamide dehydrogenase;

ww) the *E. coli* aceE gene coding for the E1 component of the pyruvate-dehydrogenase complex;

xx) the *E. coli* aceF gene coding for the E2 component of the pyruvate-dehydrogenase complex;

yy) the *E. coli* pepB gene coding for aminopeptidase B;

zz) the *E. coli* aldH gene coding for aldehyde dehydrogenase,

aaa) the *E. coli* bfr gene coding for the iron-storage homoprotein;

bbb) the *E. coli* udp gene coding for uridine phosphorylase; and

ccc) the *E. coli* rseB gene coding for the regulator of sigmaE-factor activity.

28. (Previously presented) The process of claim 21, wherein said L-amino acid is selected from the group consisting of: L-threonine; L-lysine; L-isoleucine, L-valine, L-methionine, and L-homoserine.

29. (Previously presented) The process of claim 21, wherein said L-amino acid is either L-threonine or L-lysine.

30. (Currently amended) The process of claim 28, wherein said ORF encodes a protein that consists of the amino acid sequence of SEQ ID NO:4.

31. (Previously presented) The process of claim 28, wherein some or all of the constituents of said fermentation medium and/or the biomass of said recombinant microorganism are isolated with said L-amino acid.

32. (Previously presented) The process of claim 28, wherein said ORF that encodes a protein with the amino acid sequence of SEQ ID NO:4 comprises the nucleotide sequence of SEQ ID NO:3.

33. (Previously presented) The process of claim 32 wherein said ORF that encodes a protein with the amino acid sequence of SEQ ID NO:4 consists of the nucleotide sequence of SEQ ID NO:3.

34. (Previously presented) The process of claim 28, wherein the genus of said recombinant microorganism is selected from the group consisting of: Escherichia; Erwinia; Providencia; and Serratia.

35. (Currently amended) The process of claim 28, wherein said microorganism overexpresses said ORF and, in addition, the activity of one or more additional ~~*E. coli*~~ genes is overexpressed, said one or more additional genes being selected from the group consisting of:

a) the *E. coli* thrABC operon coding for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase;
b) the *C. glutamicum* pyc gene coding for pyruvate carboxylase;
c) the *E. coli* pps gene for phosphoenolpyruvate synthase;
d) the *E. coli* ppc gene coding for phosphoenolpyruvate carboxylase;
e) the *E. coli* genes pntA and pntB coding for transhydrogenase;
f) the *E. coli* rhtB gene imparting homoserine resistance;
g) the *E. coli* mqo gene coding for malate:quinone oxidoreductase;
h) the *E. coli* rhtC gene imparting threonine resistance;
i) the *C. glutamicum* thrE gene coding for the threonine-export protein;
j) the *E. coli* gdhA gene coding for glutamate dehydrogenase;

k) the *E. coli* hns gene coding for the DNA binding protein HLP-II;

l) the *E. coli* pgm gene coding for phosphoglucomutase;

m) the *E. coli* fba gene coding for fructose biphosphate aldolase;

n) the *E. coli* ptsH gene coding for phosphohistidine protein hexose phosphotransferase;

o) the *E. coli* ptsI gene coding for enzyme I of the phosphotransferase system;

p) the *E. coli* crr gene coding for the glucose-specific IIA component;

q) the *E. coli* ptsG gene coding for the glucose-specific IIBC component;

r) the *E. coli* lrp gene coding for the regulator of the leucine regulon;

s) the *E. coli* csrA gene coding for the global regulator Csr;

t) the *E. coli* fadR gene coding for the regulator of the fad regulon;

u) the *E. coli* iclR gene coding for the regulator of central intermediary metabolism;

v) the *E. coli* mopB gene coding for the 10 kDa chaperon;

w) the *E. coli* ahpC gene coding for the small subunit of alkyl hydroperoxide reductase;

x) the *E. coli* ahpF gene coding for the large subunit of alkyl hydroperoxide reductase;

y) the *E. coli* cysK gene coding for cysteine synthase A;

z) the *E. coli* cysB gene coding for the regulator of the cys regulon;

aa) the *E. coli* cysJ gene coding for the flavoprotein of NADPH sulfite reductase;

bb) the *E. coli* cysI gene coding for the haemoprotein of NADPH sulfite reductase;

cc) the *E. coli* cysH gene coding for adenylyl sulfate reductase;

dd) the *E. coli* phoB gene coding for the positive regulator PhoB of the pho regulon;

ee) the *E. coli* phoR gene coding for the sensor protein of the pho regulon;

ff) the *E. coli* phoE gene coding for protein E of the outer cell membrane;

gg) the *E. coli* pykF gene coding for pyruvate kinase I, which is stimulated by fructose;

hh) the *E. coli* pfkB gene coding for 6-phosphofructokinase II;

ii) the *E. coli* malE gene coding for the periplasmic binding protein of maltose transport;

jj) the *E. coli* sodA gene coding for superoxide dismutase;

kk) the *E. coli* rseA gene coding for a membrane protein with anti-sigmaE activity;

ll) the *E. coli* rseC gene coding for a global regulator of the sigmaE factor;

mm) the *E. coli* sucA gene coding for the decarboxylase subunit of 2-ketoglutarate dehydrogenase;

nn) the *E. coli* sucB gene coding for the dihydrolipoyl transsuccinase E2 subunit of 2-ketoglutarate dehydrogenase;

oo) the *E. coli* sucC gene coding for the β-subunit of succinyl-CoA synthetase;

pp) the *E. coli* sucD gene coding for the α-subunit of succinyl-CoA synthetase;

qq) the *E. coli* adk gene coding for adenylate kinase;

rr) the *E. coli* hdeA gene coding for a periplasmic protein with chaperonin-type function;

ss) the *E. coli* hdeB gene coding for a periplasmic protein with chaperonin-type function;

tt) the *E. coli* icd gene coding for isocitrate dehydrogenase;

uu) the *E. coli* mglB gene coding for the periplasmic, galactose-binding transport protein;

vv) the *E. coli* lpd gene coding for dihydrolipoamide dehydrogenase;

ww) the *E. coli* aceE gene coding for the E1 component of the pyruvate-dehydrogenase complex;

xx) the *E. coli* aceF gene coding for the E2 component of the pyruvate-dehydrogenase complex;

yy) the *E. coli* pepB gene coding for aminopeptidase B;

zz) the *E. coli* aldH gene coding for aldehyde dehydrogenase,

aaa) the *E. coli* bfr gene coding for the iron-storage homoprotein;

bbb) the *E. coli* udp gene coding for uridine phosphorylase; and

ccc) the *E. coli* rseB gene coding for the regulator of sigmaE-factor activity.